

SEQUENCE LISTING

<110> Large Scale Biology Corporation
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Erwin, Robert L.
Grill, Laurence K.

<120> PRODUCTION OF LYSOSOMAL ENZYMES IN PLANTS BY TRANIENT EXPRESSION

<130> LSBC-0087-CP07B

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<151> 2001-11-13

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Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg
35 40 45

Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser
50 55 60

Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp
65 70 75 80

Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala
 85 90 95

Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe
 100 105 110

Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu
 115 120 125

Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe
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Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp
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Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu
 165 170 175

Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg
 180 185 190

Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp
 195 200 205

Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His
 210 215 220

Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser
 225 230 235 240

Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala
 245 250 255

Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe
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Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala Ile
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Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro
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Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn Gln

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Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
              20              25              30

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Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
35              40              45

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Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
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Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
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Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
85              90              95

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Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg

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Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
 385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
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Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp
      20              25              30

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Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg
35              40              45

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Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser
50              55              60

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Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp
65              70              75              80

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Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala
      85              90              95

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Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe
130 135 140

Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp
145 150 155 160

Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu
165 170 175

Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg
180 185 190

Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp
195 200 205

Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His
210 215 220

Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser
225 230 235 240

Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala
245 250 255

Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe
260 265 270

Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala Ile
275 280 285

Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro
290 295 300

Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn Gln
305 310 315 320

Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn Phe
325 330 335

Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met
 340 345 350

Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val
 355 360 365

Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr
 370 375 380

Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr Ser
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Glu Asn Thr Met Gln Met Ser Leu
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          20          25          30

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Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
          35          40          45

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```

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
          50          55          60

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Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
65          70          75          80

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Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
          85          90          95

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Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
          100          105          110

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          115          120          125

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 145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
 165 170 175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
 180 185 190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
 195 200 205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
 210 215 220

His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
 225 230 235 240

Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
 245 250 255

Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
 260 265 270

Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
 275 280 285

Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
 290 295 300

Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
 305 310 315 320

Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
 325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
 340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
 355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
 370 375 380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
 385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
 405 410 415

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 420 425 430

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 gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa 420
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 cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag 720
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<210> 12
<211> 421
<212> PRT
<213> Homo sapiens

<400> 12

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Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
20 25 30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
35 40 45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
50 55 60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
65 70 75 80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
85 90 95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
100 105 110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
115 120 125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
130 135 140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
 145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
 165 170 175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
 180 185 190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
 195 200 205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
 210 215 220

His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
 225 230 235 240

Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
 245 250 255

Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
 260 265 270

Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
 275 280 285

Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
 290 295 300

Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
 305 310 315 320

Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
 325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
 340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
 355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile

370

375

380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
 385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
 405 410 415

Leu Glu Asn Thr Met
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<210> 13
 <211> 1284
 <212> DNA
 <213> Homo sapiens

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 accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca 180
 gattcctgca tcagtggaga gctcttcatg gagatggcag agctcatggt ctcagaaggc 240
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 gattcagaag gcagacttca ggcagaccct cagcgctttc ctcatgggat tcgccagcta 360
 gctaattatg ttcacagcaa aggactgaag ctagggtatt atgcagatgt tggaaataaa 420
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 gactggggag tagatctgct aaaatttgat ggttggtact gtgacagttt ggaaaatttg 540
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 agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg 780
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<210> 14
 <211> 427
 <212> PRT
 <213> Homo sapiens

<400> 14

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Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
 20 25 30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
 85 90 95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
 100 105 110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
 115 120 125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
 130 135 140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
 145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser

165	170	175
Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn		
180	185	190
Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met		
195	200	205
Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn		
210	215	220
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys		
225	230	235
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val		
245	250	255
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn		
260	265	270
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala		
275	280	285
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser		
290	295	300
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn		
305	310	315
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn		
325	330	335
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala		
340	345	350
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala		
355	360	365
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile		
370	375	380
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr		
385	390	395
		400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
405 410 415

Leu Glu Asn Thr Met Ser Glu Lys Asp Glu Leu
420 425

<210> 15
<211> 1254
<212> DNA
<213> Homo sapiens

<400> 15
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accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca 180
gattcctgca tcagtgagaa gctcttcatg gagatggcag agctcatggt ctcagaaggc 240
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gattcagaag gcagacttca ggcagaccct cagcgctttc ctcatgggat tcgccagcta 360
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acctgcgcag gcttccttgg gagttttgga tactacgaca ttgatgcca gacctttgct 480
gactggggag tagatctgct aaaatttgat ggttggttact gtgacagttt ggaaaatttg 540
gcagatgggtt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac 600
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agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg 780
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gtaactcaga tggccctctg ggctatcatg gctgctcctt tattcatgtc taatgacctc 900
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tcaagggttaa gaagtcacat aaatcccaca ggcactggtt tgcttcagct ataa 1254

<210> 16
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 16

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu
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Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
 20 25 30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
 85 90 95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
 100 105 110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
 115 120 125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
 130 135 140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
 145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
 165 170 175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
 180 185 190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
 195 200 205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
 210 215 220

His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
 225 230 235 240

Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
 245 250 255

Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
 260 265 270

Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
 275 280 285

Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
 290 295 300

Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
 305 310 315 320

Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
 325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
 340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
 355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
 370 375 380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
 385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
 405 410 415

Leu

<210> 17
 <211> 1272
 <212> DNA
 <213> Homo sapiens

<400> 17
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 accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca 180
 gattcctgca tcagtgagaa gctcttcatg gagatggcag agctcatggt ctcagaaggc 240
 tggaaggatg caggttatga gtacctctgc attgatgact gttggatggc tcccaaaga 300
 gattcagaag gcagacttca ggcagacct cagcgcttcc ctcattggat tcgccagcta 360
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 gactggggag tagatctgct aaaatttgat ggttggtact gtgacagttt ggaaaatttg 540
 gcagatgggt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac 600
 tcctgtgagt ggccctctta tatgtggccc ttcaaaagc ccaattatac agaaatccga 660
 cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag 720
 agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg 780
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 gcctgcttca tcacacagct cctccctgtg aaaaggaagc tagggttcta tgaatggact 1200
 tcaagggtta gaagtcacat aaatcccaca ggcactgttt tgcttcagct atctgaaaag 1260
 gacgaattat ga 1272

<210> 18
 <211> 423
 <212> PRT

<213> Homo sapiens

<400> 18

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20 25 30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
35 40 45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
50 55 60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
65 70 75 80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
85 90 95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
100 105 110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
115 120 125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
130 135 140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
165 170 175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
180 185 190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
195 200 205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn

210	215	220
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys		
225	230	235 240
Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val		
	245	250 255
Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn		
	260	265 270
Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala		
	275	280 285
Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser		
	290	295 300
Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn		
	305	310 315 320
Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn		
	325	330 335
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala		
	340	345 350
Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala		
	355	360 365
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile		
	370	375 380
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr		
	385	390 395 400
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln		
	405	410 415
Leu Ser Glu Lys Asp Glu Leu		
	420	

<210> 19
 <211> 1215

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<212> DNA
<213> Homo sapiens

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accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca      180
gattcctgca tcagtgagaa gctcttcatg gagatggcag agctcatggg ctcagaaggc      240
tggaaggatg caggttatga gtacctctgc attgatgact gttggatggc tccccaaaga      300
gattcagaag gcagacttca ggcagaccct cagcgctttc ctcatgggat tcgccagcta      360
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gactggggag tagatctgct aaaatttgat gggtgttact gtgacagttt ggaaaatttg      540
gcagatgggt ataagcacat gtccctggcc ctgaatagga ctggcagaag cattgtgtac      600
tcctgtgagt ggccctctta tatgtggccc ttcaaaaagc ccaattatac agaaatccga      660
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cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tgccatcaat      960
caggaccctt tgggcaagca agggtagcag cttagacagg gagacaactt tgaagtgtgg     1020
gaacgacctc tctcaggctt agcctgggct gtagctatga taaaccggca ggagattggg     1080
ggacctcgct cttataccat cgcagttgct tcctgggta aaggagtggc ctgtaatcct     1140
gcctgcttca tcacacagct cctccctgtg aaaaggaagc tagggttcta tgaatggact     1200
tcaagggttaa gataa                                           1215

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<210> 20
<211> 401
<212> PRT
<213> Homo sapiens

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<400> 20

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Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg Phe Leu
1          5          10          15

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 20 25 30

Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg Phe Met
 35 40 45

Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser Glu Lys
 50 55 60

Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp Lys Asp
 65 70 75 80

Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala Pro Gln
 85 90 95

Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe Pro His
 100 105 110

Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu Lys Leu
 115 120 125

Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe Pro Gly
 130 135 140

Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp Trp Gly
 145 150 155 160

Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu Glu Asn
 165 170 175

Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg Thr Gly
 180 185 190

Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp Pro Phe
 195 200 205

Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His Trp Arg
 210 215 220

Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser Ile Leu
 225 230 235 240

Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala Gly Pro
 245 250 255

Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe Gly Leu
 260 265 270

Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala Ile Met Ala
 275 280 285

Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro Gln Ala
 290 295 300

Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn Gln Asp Pro
 305 310 315 320

Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn Phe Glu Val
 325 330 335

Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met Ile Asn
 340 345 350

Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val Ala Ser
 355 360 365

Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr Gln Leu
 370 375 380

Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr Ser Arg Leu
 385 390 395 400

Arg

<210> 21
 <211> 1233
 <212> DNA
 <213> Homo sapiens

<400> 21
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 accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca 180
 gattcctgca tcagtgaaga gctcttcatg gagatggcag agctcatggc ctcagaaggc 240

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gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa    420
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gactggggag tagatctgct aaaatttgat ggttggtact gtgacagttt ggaaaatttg    540
gcagatgggt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac    600
tcctgtgagt ggctcttcta tatgtggccc tttcaaaagc ccaattatac agaaatccga    660
cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag    720
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gcctgcttca tcacacagct cctccctgtg aaaaggaagc tagggttcta tgaatggact   1200
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<210> 22
<211> 409
<212> PRT
<213> Homo sapiens

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<400> 22
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Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg
1           5           10           15

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Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp
20           25           30

```

```

Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg
35           40           45

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Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser
50           55           60

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Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly Trp
 65 70 75 80

Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met Ala
 85 90 95

Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg Phe
 100 105 110

Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu
 115 120 125

Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe
 130 135 140

Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp
 145 150 155 160

Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser Leu
 165 170 175

Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn Arg
 180 185 190

Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met Trp
 195 200 205

Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn His
 210 215 220

Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser
 225 230 235 240

Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala
 245 250 255

Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe
 260 265 270

Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala Ile
 275 280 285

Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser Pro
 290 295 300

Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn Gln
 305 310 315 320

Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn Phe
 325 330 335

Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met
 340 345 350

Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val
 355 360 365

Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr
 370 375 380

Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr Ser
 385 390 395 400

Arg Leu Arg Ser Glu Lys Asp Glu Leu
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<210> 23
 <211> 30
 <212> PRT
 <213> Tobacco mosaic virus

<400> 23

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu
 1 5 10 15

Gln Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu
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<210> 24
 <211> 36
 <212> PRT
 <213> Tobacco mosaic virus

<400> 24

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu
 1 5 10 15

Gln Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu Ser Glu
20 25 30

Lys Asp Glu Leu
35

<210> 25
<211> 26
<212> PRT
<213> Tobacco mosaic virus

<400> 25

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu
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Gln Leu Glu Asn Thr Met Gln Met Ser Leu
20 25

<210> 26
<211> 32
<212> PRT
<213> Tobacco mosaic virus

<400> 26

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu
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Gln Leu Glu Asn Thr Met Gln Met Ser Leu Ser Glu Lys Asp Glu Leu
20 25 30

<210> 27
<211> 22
<212> PRT
<213> Tobacco mosaic virus

<400> 27

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu
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Gln Leu Glu Asn Thr Met
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<210> 28
<211> 29

<212> PRT
<213> Tobacco mosaic virus

<400> 28

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Leu Gln Leu Glu Asn Thr Met Ser Glu Lys Asp Glu Leu
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<210> 29
<211> 18
<212> PRT
<213> Tobacco mosaic virus

<400> 29

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu
1 5 10 15

Gln Leu

<210> 30
<211> 24
<212> PRT
<213> Tobacco mosaic virus

<400> 30

Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu
1 5 10 15

Gln Leu Ser Glu Lys Asp Glu Leu
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<210> 31
<211> 5
<212> PRT
<213> Tobacco mosaic virus

<400> 31

Thr Ser Arg Leu Arg
1 5

<210> 32
<211> 11
<212> PRT

<213> Tobacco mosaic virus

<400> 32

Thr	Ser	Arg	Leu	Arg	Ser	Glu	Lys	Asp	Glu	Leu
1				5					10	